

What is claimed:

1. An assay for the identification an antibiotic comprising:
 - (a) contacting an assay composition comprising a CoaX protein with a test compound; and
 - (b) determining the ability of the test compound to inhibit the activity of the CoaX protein;wherein the compound is identified as an antibiotic based on the ability of the compound to inhibit the activity of the CoaX protein.
2. The assay of claim 1, wherein the assay composition comprises purified CoaX protein.
3. The assay of claim 1, wherein the assay composition comprises partially purified CoaX protein.
4. The assay of claim 1, wherein the assay composition comprises crude cell extracts from a cell producing CoaX protein.
5. The assay of claim 1, wherein the CoaX protein is encoded by a *coaX* gene derived from a pathogenic bacteria selected from the group consisting of *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Clostridium difficile*, *Helicobacter pylori*, *Neisseria meningitidis*, *Pseudomonas aeruginosa*, *Treponema pallidum* and *Xylella fastidiosa*.
6. The assay of claim 5, wherein the CoaX protein has an amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:55, SEQ ID NO:14 or SEQ ID NO:67, SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:20, SEQ ID NO:10 and SEQ ID NO:65.
7. The assay of claim 1, wherein the CoaX protein is encoded by a *coaX* gene derived from a pathogenic bacteria selected from the group consisting of *Bacillus anthracis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Clostridium difficile*, *Helicobacter pylori*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Porphyromonas gingivalis*, *Pseudomonas aeruginosa*, *Treponema pallidum* and *Xylella fastidiosa*.

8. The assay of claim 7, wherein the CoaX protein has an amino acid sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:15, SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:55, SEQ ID NO:14 or SEQ ID NO:67, SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:20, SEQ ID NO:10 and SEQ ID NO:65.

9. The assay of claim 1, wherein the CoaX is encoded by a *coaX* gene derived from a bacteria selected from the group consisting of *Aquifex aeolicus*, *Bacillus anthracis*, *Bacillus halodurans*, *Bacillus stearothermophilus*, *Bacillus subtilis*, *Caulobacter crescentus*, *Chlorobium tepidum*, *Clostridium acetobutylicum*, *Dehalococcoides ethenogenes*, *Deinococcus radiodurans*, *Desulfovibrio vulgaris*, *Geobacter sulfurreducens*, *Pseudomonas putida*, *Rhodobacter capsulatus*, *Thiobacillus ferrooxidans*, *Streptomyces coelicolor*, *Synechocystis* sp., *Thermotoga maritima*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Clostridium difficile*, *Helicobacter pylori*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Porphyromonas gingivalis*, *Pseudomonas aeruginosa*, *Treponema pallidum*, *Xylella fastidiosa* and *Mycobacterium tuberculosis*.

10. The assay of claim 9, wherein the CoaX protein has an amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:70, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:3, SEQ ID NO:57, SEQ ID NO:8, SEQ ID NO:59, SEQ ID NO:7, SEQ ID NO:61, SEQ ID NO:6, SEQ ID NO:63, SEQ ID NO:4, SEQ ID NO:13, SEQ ID NO:9, SEQ ID NO:15, SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:55, SEQ ID NO:14 or SEQ ID NO:67, SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:20, SEQ ID NO:10, SEQ ID NO:65 and SEQ ID NO:5.

11. The assay of claim 1, wherein said composition is further contacted with pantothenate or a pantothenate analog.

12. The assay of claim 11, wherein the ability to modulate activity of CoaX is determined based on the ability of the test compound to effect levels of pantothenate or pantothenate analog in the assay mixture.

13. An assay for the identification a potential antibiotic comprising:
(a) contacting an assay composition comprising CoaX with a test compound;
and

(b) determining the ability of the test compound to bind to the CoaX;
wherein the compound is identified as a potential antibiotic based on the
ability of the compound to bind to the CoaX.

5 14. An assay for the identification an antibiotic comprising:
 (a) contacting an assay composition comprising CoaX with a test compound;
 (b) determining the ability of the test compound to bind to the CoaX;
 (c) selecting the test compound as a potential antibiotic based the ability to
 bind to the CoaX; and
10 (d) further determining the ability of the selected compound to inhibit the
 activity of a CoaX;
 wherein the compound is identified as a potential antibiotic based on the
 ability of the compound to bind to the CoaX.

15 15. An assay for the identification a potential antibiotic comprising:
 (a) contacting an assay composition comprising CoaX with a test compound
 and pantothenate or a pantothenate analog; and
 (b) determining the ability of the test compound to modulate binding of the
 pantothenate or pantothenate analog to the CoaX;
20 wherein the compound is identified as a potential antibiotic based on the
 ability of the compound to modulate binding of the pantothenate or pantothenate analog
 to the CoaX.

25 16. An assay for the identification an antibiotic comprising:
 (a) contacting an assay composition comprising CoaX with a test compound
 and pantothenate or a pantothenate analog;
 (b) determining the ability of the test compound to modulate binding of the
 pantothenate or pantothenate analog to the CoaX;
 (c) selecting the test compound as a potential antibiotic based the ability to
30 modulate binding of the pantothenate or pantothenate analog to the
 CoaX; and
 (d) further determining the ability of the selected compound to inhibit the
 activity of a CoaX;
 wherein the compound is identified as a potential antibiotic based on the
35 ability of the compound to bind to the CoaX.

17. A method for identifying compounds which modulate pantothenate kinase activity comprising contacting a recombinant cell expressing a single pantothenate kinase encoded by a *coaX* gene with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in said cell.

18. A method for identifying compounds which modulate pantothenate kinase activity comprising contacting a recombinant cell expressing a first and second pantothenate kinase, with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in said cell, wherein the first or second pantothenate kinase has reduced activity.

19. The method of claim 18, wherein said first pantothenate kinase is encoded by a *coaA* gene and said second pantothenate kinase is encoded by a *coaX* gene.

20. The method of claim 18, wherein said first pantothenate kinase is encoded by a *coaX* gene and said second pantothenate kinase is encoded by a *coaA* gene.

21. The method of claim 18, wherein said recombinant cell is a Gram negative microorganism

22. The method of claim 18, wherein said recombinant cell is a Gram positive microorganism

23. The method of claim 18, wherein the microorganism is of the genus *Bacillus* or *Escherchia*.

24. The method of claim 18, wherein the microorganism is *Bacillus subtilis* or *Escherchia coli*.

25. The method of claim 18, wherein determining the ability of the test compound to modulate pantothenate kinase activity in said cell comprises determining the ability of the test compound to inhibit pantothenate kinase activity.

26. An isolated nucleic acid molecule comprising a *coaX* gene.

27. An isolated pantothenate kinase protein encoded by a *coaX* gene.

5 28. The pantothenate kinase of claim 27, which is encoded by a *coaX* gene derived from a pathogenic bacteria selected from the group consisting of *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Helicobacter pylori*, *Neisseria meningitidis*, *Pseudomonas aeruginosa*, *Treponema pallidum* and *Xylella fastidiosa*.

10 29. The pantothenate kinase of claim 28, having an amino acid sequence selected from the group consisting of SEQ ID NO:15, SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:14 or SEQ ID NO:67, SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:20, SEQ ID NO:10 and SEQ ID NO:65.

15 30. The pantothenate kinase of claim 27, which is encoded by a *coaX* gene derived from a pathogenic bacteria selected from the group consisting of *Bacillus anthracis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Clostridium difficile*, *Helicobacter pylori*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Porphyromonas gingivalis*, *Pseudomonas aeruginosa*, *Treponema pallidum* and *Xylella fastidiosa*.

20 31. The pantothenate kinase of claim 30, having an amino acid sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:15, SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:55, SEQ ID NO:14 or SEQ ID NO:67, SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:20, SEQ ID NO:10 and SEQ ID NO:65.

30 32. The pantothenate kinase of claim 27, which is encoded by a *coaX* gene derived from a bacteria selected from the group consisting of *Aquifex aeolicus*, *Bacillus anthracis*, *Bacillus halodurans*, *Bacillus stearothermophilus*, *Bacillus subtilis*, *Caulobacter crescentus*, *Chlorobium tepidum*, *Clostridium acetobutylicum*, *Dehalococcoides ethenogenes*, *Deinococcus radiodurans*, *Desulfovibrio vulgaris*, *Geobacter sulfurreducens*, *Pseudomonas putida*, *Rhodobacter capsulatus*, *Thiobacillus ferrooxidans*, *Streptomyces coelicolor*, *Synechocystis sp.*, *Thermotoga maritima*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Campylobacter jejuni*, *Clostridium difficile*, *Helicobacter pylori*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Porphyromonas*

gingivalis, *Pseudomonas aeruginosa*, *Treponema pallidum*, *Xylella fastidiosa* and *Mycobacterium tuberculosis*.

33. The pantothenate kinase of claim 32, having an amino acid
5 sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:45, SEQ ID
NO:47, SEQ ID NO:49, SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:3,
SEQ ID NO:57, SEQ ID NO:8, SEQ ID NO:59, SEQ ID NO:7, SEQ ID NO:61, SEQ ID
NO:6, SEQ ID NO:63, SEQ ID NO:4, SEQ ID NO:13, SEQ ID NO:9, SEQ ID NO:15,
SEQ ID NO:11, SEQ ID NO:21, SEQ ID NO:55, SEQ ID NO:14 or SEQ ID NO:67,
10 SEQ ID NO:43 or SEQ ID NO:22, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:20,
SEQ ID NO:10, SEQ ID NO:65 and SEQ ID NO:5

34. A recombinant vector comprising an isolated *coaX* gene.

- 15 35. A recombinant microorganism comprising the vector of claim 34.

36. A recombinant microorganism selected from the group consisting
of PA861, PA876, YH1 comprising pOTP71, YH1 comprising pOTP72, YH1
comprising pOTP73, and YH1 comprising pAN341.

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